

SEQUENCE LISTING

<110> Fainzilber, Michael M.  
Kits, Karel S.  
Burlingame, Alma L.  
Olivera, Baldomero M.  
Walker, Craig  
Watkins, Maren  
Shetty, Reshma  
Cruz, Lourdes J.  
Imperial, Julita  
Colledge, Clark  
University of Utah Research Foundation  
Vrije Universiteit  
Regents of the University of California

<120> Gamma-Conopeptides

<130> 2314-147-sq2

<140>

<141>

<150> US 60/069,706

<151> 1997-12-16

<160> 47

<170> PatentIn Ver. 2.0

<210> 1

<211> 42

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:generic formula  
of gamma-conopeptides

<220>

<221> PEPTIDE

<222> (1)..(13)

<223> Xaa at residues 1, 2, 3, 4, 5, and 6 may be  
des-Xaa or any amino acid; Xaa at residues 8, 9,  
10, 11 and 12 may be any amino acid; Xaa at  
residue 13 may be des-Xaa or any amino acid.

<220>

<221> PEPTIDE

<222> (15)..(19)

<223> Xaa at residues 15, 16, 17 and 18 may be any amino  
acid; Xaa at residue 19 is Glu,  
gamma-carboxyglutamate or Gln.

<220>

<221> PEPTIDE

<222> (22)..(28)

<223> Xaa at residues 22, 23 and 24 may be any amino  
acid; Xaa at residue 25 may be des-Xaa or any  
amino acid; Xaa at residues 27, 28 and 29 may be  
any amino acid.

<220>

<221> PEPTIDE

<222> (30)..(42)

<223> Xaa at residues 30, 31 and 32 may be des-Xaa or any amino acid; Xaa at residues 34, 35, 36, 37, 38, 39, 40, 41 and 42 may be des-Xaa or any amino acid.

<400> 1

Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa  
1 5 10 15

Xaa Xaa Xaa Cys Cys Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa  
20 25 30

Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
35 40

<210> 2

<211> 42

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:generic sequence of gamma-conopeptides.

<220>

<221> PEPTIDE

<222> (1)..(13)

<223> Xaa at residues 1, 2, 3, 4, 5 and 6 may be des-Xaa or any amino acid; Xaa at residues 8, 9, 10, 11 and 12 may be any amino acid; Xaa at residue 13 may be des-Xaa or any amino acid.

<220>

<221> PEPTIDE

<222> (15)..(22)

<223> Xaa at residues 15, 16, 17 and 18 may be any amino acid; Xaa at residue 19 is Glu, gamma-carboxyglutamate or Gln; Xaa at residue 22 is Ser or Thr.

<220>

<221> PEPTIDE

<222> (23)..(29)

<223> Xaa at residues 23 and 24 may be any amino acid; Xaa at residue 25 may be des-Xaa or any amino acid; Xaa at residues 27, 28 and 29 may be any amino acid.

<220>

<221> PEPTIDE

<222> (30)..(42)

<223> Xaa at residues 30, 31 and 32 may be des-Xaa or any amino acid; Xaa at residues 34, 35, 36, 37, 38, 39, 40, 41 and 42 may be des-Xaa or any amino acid.

<400> 2

Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa  
1 5 10 15

Xaa Xaa Xaa Cys Cys Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa  
20 25 30

Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
35 40

<210> 3  
<211> 39  
<212> PRT  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence:generic formula  
of gamma-conopeptides

<220>  
<221> PEPTIDE  
<222> (1)..(13)  
<223> Xaa at residue 1 is any amino acid; Xaa at  
residues 2, 3, 4, 5 and 6 may be des-Xaa or any  
amino acid; Xaa at residues 8, 9, 10, 11, 12 and  
13 may be any amino acid.

<220>  
<221> PEPTIDE  
<222> (27)..(39)  
<223> Xaa at residues 27, 28, 29, 31, 32, 33, 34, 35, 36  
and 37 may be any amino acid; Xaa at residues 38  
and 39 may be des-Xaa or any amino acid.

<220>  
<221> PEPTIDE  
<222> (15)..(19)  
<223> Xaa at residues 15, 16, 17 and 18 may be any amino  
acid; Xaa at residue 19 is Glu or  
gamma-carboxyglutamate.

<400> 3  
Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa  
1 5 10 15

Xaa Xaa Xaa Cys Cys Ser Asn Ser Cys Asp Xaa Xaa Xaa Cys Xaa Xaa  
20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
35

<210> 4  
<211> 39  
<212> PRT  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence:generic  
sequence of gamma-conopeptides.  
  
<220>  
<221> PEPTIDE  
<222> (1)..(13)  
<223> Xaa at residue 1 is any amino acid; Xaa at  
residues 2, 3, 4, 5 and 6 may be des-Xaa or any  
amino acid; Xaa at residues 8, 9, 10, 11, 12 and  
13 may be any amino acid.

<220>

<221> PEPTIDE  
<222> (15)..(19)  
<223> Xaa at residue 15 is Ser or Thr; Xaa at residues 16, 17 and 18 may be any amino acid; Xaa at residue 19 is Glu or gamma-carboxyglutamate.

<220>  
<221> PEPTIDE  
<222> (27)..(39)  
<223> Xaa at residues 27, 28, 29, 31, 32, 33, 34, 35, 36 and 37 may be any amino acid; Xaa at residues 38 and 39 may be des-Xaa or any amino acid.

<400> 4  
Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa  
1 5 10 15  
Xaa Xaa Xaa Cys Cys Ser Asn Ser Cys Asp Xaa Xaa Xaa Cys Xaa Xaa  
20 25 30  
Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
35

<210> 5  
<211> 34  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:generic sequence of gamma-conopeptides.

<220>  
<221> PEPTIDE  
<222> (1)..(6)  
<223> Xaa at residues 1 and 2 may be des-Xaa or any amino acid; Xaa at residue 3 is Asp, Glu or gamma-carboxyglutamate; Xaa at residues 5 and 6 may be any amino acid.

<220>  
<221> PEPTIDE  
<222> (7)..(16)  
<223> Xaa at residue 7 is Trp or 6-bromo-Trp; Xaa at residues 9; 10, 13 and 14 may be any amino acid; Xaa at residue 16 is Glu or gamma-carboxyglutamate.

<220>  
<221> PEPTIDE  
<222> (28)..(34)  
<223> Xaa at residues 28, 30, 31, 32, 33 and 34 may be any amino acid.

<400> 5  
Xaa Xaa Xaa Cys Xaa Xaa Xaa Phe Xaa Xaa Cys Thr Xaa Xaa Ser Xaa  
1 5 10 15  
Cys Cys Ser Asn Ser Cys Asp Gln Thr Tyr Cys Xaa Leu Xaa Xaa Xaa  
20 25 30  
Xaa Xaa

<210> 6  
<211> 32  
<212> PRT  
<213> Conus pennaceus

<220>  
<221> PEPTIDE  
<222> (1)..(31)  
<223> Xaa at residue 5 is Trp or 6-bromo-Trp; Xaa at residues 14 and 26 are Glu or gamma-carboxyglutamate; Xaa at residue 31 is Pro or hydroxy-Pro.

<400> 6  
Asp Cys Thr Ser Xaa Phe Gly Arg Cys Thr Val Asn Ser Xaa Cys Cys  
1 5 10 15  
Ser Asn Ser Cys Asp Gln Thr Tyr Cys Xaa Leu Tyr Ala Phe Xaa Ser  
20 25 30

<210> 7  
<211> 34  
<212> PRT  
<213> Conus textile

<220>  
<221> PEPTIDE  
<222> (1)..(34)  
<223> Xaa at residues 1, 7 and 34 are Trp or 6-bromo-Trp; Xaa at residues 3 and 16 are Glu or gamma-carboxyglutamate; Xaa at residues 31 and 32 are Pro or hydroxy-Pro.

<400> 7  
Xaa Leu Xaa Cys Ser Val Xaa Phe Ser His Cys Thr Lys Asp Ser Xaa  
1 5 10 15  
Cys Cys Ser Asn Ser Cys Asp Gln Thr Tyr Cys Thr Leu Met Xaa Xaa  
20 25 30  
Asp Xaa

<210> 8  
<211> 39  
<212> PRT  
<213> Conus textile

<220>  
<221> PEPTIDE  
<222> (1)..(39)  
<223> Xaa at residues 1, 2, 4, 10 and 39 are Trp or 6-bromo-Trp ; Xaa at residues 19 and 31 are Glu or gamma-carboxyglutamate; Xaa at residues 34, 36 and 37 are Pro or hydroxy-Pro.

<400> 8  
Xaa Xaa Arg Xaa Gly Gly Cys Met Ala Xaa Phe Gly Leu Cys Ser Arg

1

5

10

15

Asp Ser Xaa Cys Cys Ser Asn Ser Cys Asp Val Thr Arg Cys Xaa Leu  
20 25 30

Met Xaa Phe Xaa Xaa Asp Xaa  
35

<210> 9  
<211> 27  
<212> PRT  
<213> Conus textile

<220>  
<221> PEPTIDE  
<222> (1)..(27)  
<223> Xaa at residues 9, 13 and 17 are Glu or  
gamma-carboxyglutamate.

<400> 9  
Cys Lys Thr Tyr Ser Lys Tyr Cys Xaa Ala Asp Ser Xaa Cys Cys Thr  
1 5 10 15

Xaa Gln Cys Val Arg Ser Tyr Cys Thr Leu Phe  
20 25

<210> 10  
<211> 34  
<212> PRT  
<213> Conus textile

<220>  
<221> PEPTIDE  
<222> (1)..(34)  
<223> Xaa at residues 2, 3, 10 and 32 are Trp or  
6-bromo-Trp; Xaa at residues 18, 26 and 33 are Glu  
or gamma-carboxyglutamate; Xaa at residue 12 is  
Pro or hydroxy-Pro.

<400> 10  
Asp Xaa Xaa Asp Asp Gly Cys Ser Val Xaa Gly Xaa Cys Thr Tyr Asn  
1 5 10 15

Ala Xaa Cys Cys Ser Gly Asp Cys His Xaa Thr Cys Ile Phe Gly Xaa  
20 25 30

Xaa Val

<210> 11  
<211> 31  
<212> PRT  
<213> Conus textile

<220>  
<221> PEPTIDE  
<222> (1)..(31)  
<223> Xaa at residues 3 and 31 are Trp of 6-bromo-Trp;  
Xaa at residues 5, 18, 22 and 25 are Glu or  
gamma-carboxyglutamate; Xaa at residue 16 is Pro  
or hydroxy-Pro.

<400> 11  
Gly Met Xaa Gly Xaa Cys Lys Asp Gly Leu Thr Thr Cys Leu Ala Xaa  
1 5 10 15  
Ser Xaa Cys Cys Ser Xaa Asp Cys Xaa Gly Ser Cys Thr Met Xaa  
20 25 30

<210> 12  
<211> 32  
<212> PRT  
<213> Conus gloriamaris

<220>  
<221> PEPTIDE  
<222> (1)..(32)  
<223> Xaa at residue 5 is Trp or 6-bromo-Trp; Xaa at  
residue 1 is Glu or gamma-carboxyglutamate; Xaa at  
residues 8 and 11 are Pro or hydroxy-Pro.

<400> 12  
Xaa Cys Arg Ala Xaa Tyr Ala Xaa Cys Ser Xaa Gly Ala Gln Cys Cys  
1 5 10 15  
Ser Leu Leu Met Cys Ser Lys Ala Thr Ser Arg Cys Ile Leu Ala Leu  
20 25 30

<210> 13  
<211> 29  
<212> PRT  
<213> Conus marmoreus

<220>  
<221> PEPTIDE  
<222> (1)..(29)  
<223> Xaa at residues 8 and 15 are Trp or 6-bromo-Trp;  
Xaa at residues 5, 16 and 23 are Glu or  
gamma-carboxyglutamate; Xaa at residue 10 is Pro  
or hydroxy-Pro.

<400> 13  
Asn Gly Gln Cys Xaa Asp Val Xaa Met Xaa Cys Thr Ser Asn Xaa Xaa  
1 5 10 15  
Cys Cys Ser Leu Asp Cys Xaa Met Tyr Cys Thr Gln Ile  
20 25

<210> 14  
<211> 27  
<212> PRT  
<213> Conus marmoreus

<220>  
<221> PEPTIDE  
<222> (1)..(27)  
<223> Xaa at residue 4 is Trp or 6-bromo-Trp; Xaa at  
residues 9, 12, 13 and 17 are Glu or  
gamma-carboxyglutamate.

<400> 14  
Cys Gly Gly Xaa Ser Thr Tyr Cys Xaa Val Asp Xaa Xaa Cys Cys Ser  
1 5 10 15  
Xaa Ser Cys Val Arg Ser Tyr Cys Thr Leu Phe  
20 25

<210> 15  
<211> 26  
<212> PRT  
<213> Conus marmoreus

<220>  
<221> PEPTIDE  
<222> (1)..(26)  
<223> Xaa at residues 8 and 15 are Trp or 6-bromo-Trp;  
Xaa at residue 16 is Glu or  
gamma-carboxyglutamate.

<400> 15  
Asn Gly Gly Cys Lys Ala Thr Xaa Met Ser Cys Ser Ser Gly Xaa Xaa  
1 5 10 15  
Cys Cys Ser Met Ser Cys Asp Met Tyr Cys  
20 25

<210> 16  
<211> 323  
<212> DNA  
<213> Conus textile

<220>  
<221> CDS  
<222> (1)..(153)

<400> 16  
gaa cgg gct aag atc aac ttg ctt cca aag aga aag cca cct gct gag 48  
Glu Arg Ala Lys Ile Asn Leu Leu Pro Lys Arg Lys Pro Pro Ala Glu  
1 5 10 15

cgt tgg ttg gaa tgc agt gtt tgg ttt tca cat tgt acg aag gac tcg 96  
Arg Trp Leu Glu Cys Ser Val Trp Phe Ser His Cys Thr Lys Asp Ser  
20 25 30

gaa tgt tgt tct aat agt tgt gac caa acg tac tgc acg tta atg cca 144  
Glu Cys Cys Ser Asn Ser Cys Asp Gln Thr Tyr Cys Thr Leu Met Pro  
35 40 45

ccg gac tgg tgacatcgcc actctcctgt tcagagtctt caaggcttt 193  
Pro Asp Trp  
50

gttctctttt gaagaatttt aacgagtgaa caaaaaagtg gactagcatg tttcctttc 253  
ccttgcaaa atcaatgatg gaggtaaaag cctcccatc tgtcttcatc aataaagaac 313  
ttatcatcat 323

<210> 17  
<211> 51  
<212> PRT

<213> Conus textile

<400> 17

Glu Arg Ala Lys Ile Asn Leu Leu Pro Lys Arg Lys Pro Pro Ala Glu  
1 5 10 15

Arg Trp Leu Glu Cys Ser Val Trp Phe Ser His Cys Thr Lys Asp Ser  
20 25 30

Glu Cys Cys Ser Asn Ser Cys Asp Gln Thr Tyr Cys Thr Leu Met Pro  
35 40 45

Pro Asp Trp  
50

<210> 18

<211> 510

<212> DNA

<213> Conus textile

<220>

<221> CDS

<222> (95)..(337)

<400> 18

tgactcgcca tctcctctct cagtctccct gacagctgcc ttcagtcgac cctgcccgtca 60

tctcaacgca cacttgaagt gaaaaacctt tatac atg gag aaa ctg aca att ctg 115  
Met Glu Lys Leu Thr Ile Leu  
1 5

ctt ctt gtt gct gta ctg ttg tcg atc cag gcc cta aat caa gaa 163  
Leu Leu Val Ala Ala Val Leu Leu Ser Ile Gln Ala Leu Asn Gln Glu  
10 15 20

aaa cac caa cgg gca aag atc aac ttg ctt tca aag aga aag cca cct 211  
Lys His Gln Arg Ala Lys Ile Asn Leu Leu Ser Lys Arg Lys Pro Pro  
25 30 35

gct gag cgt tgg tgg cgg tgg gga tgc atg gct tgg ttt ggg ctt 259  
Ala Glu Arg Trp Trp Arg Trp Gly Gly Cys Met Ala Trp Phe Gly Leu  
40 45 50 55

tgt tcg agg gac tcg gaa tgt tgt tct aat agt tgt gac gta acg cgc 307  
Cys Ser Arg Asp Ser Glu Cys Cys Ser Asn Ser Cys Asp Val Thr Arg  
60 65 70

tgc gag tta atg cca ttc cca cca gac tgg tgacatcgac actctcctct 357  
Cys Glu Leu Met Pro Phe Pro Asp Trp  
75 80

tcagagtctt caaggctttt gttctctttt gaagaatttt tacgagtgaa caaaaacgtg 417

gactagcacg tttccttttc ccttgcaaa atcaatgatg gaggtaaaag tgtcccattt 477

tgtcttcatc aataaagaac ttatcatcat aat 510

<210> 19

<211> 81

<212> PRT

<213> Conus textile

<400> 19  
Met Glu Lys Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Leu Ser  
1 5 10 15  
  
Ile Gln Ala Leu Asn Gln Glu Lys His Gln Arg Ala Lys Ile Asn Leu  
20 25 30  
  
Leu Ser Lys Arg Lys Pro Pro Ala Glu Arg Trp Trp Arg Trp Gly Gly  
35 40 45  
  
Cys Met Ala Trp Phe Gly Leu Cys Ser Arg Asp Ser Glu Cys Cys Ser  
50 55 60  
  
Asn Ser Cys Asp Val Thr Arg Cys Glu Leu Met Pro Phe Pro Pro Asp  
65 70 75 80  
  
Trp

<210> 20  
<211> 441  
<212> DNA  
<213> Conus textile

<220>  
<221> CDS  
<222> (16)..(243)

<400> 20  
ggaaaaactt ttatc atg gag aaa ctg aca atc ctg ctc ctt gtt gct gct 51  
Met Glu Lys Leu Thr Ile Leu Leu Leu Val Ala Ala  
1 5 10  
  
gta ctg atg tcg acc cag gcc atg ttt caa ggt gat gga gaa aaa tcc 99  
Val Leu Met Ser Thr Gln Ala Met Phe Gln Gly Asp Gly Glu Lys Ser  
15 20 25  
  
cg<sup>g</sup> aag g<sup>g</sup>c<sup>g</sup> gag atc aac ttt tct gaa aca aga aag ttg g<sup>g</sup>c<sup>g</sup> aga aac 147  
Arg Lys Ala Glu Ile Asn Phe Ser Glu Thr Arg Lys Leu Ala Arg Asn  
30 35 40  
  
aag cag aaa cgc tgc aaa act tat tca aag tat tgt gaa gct gac tcg 195  
Lys Gln Lys Arg Cys Lys Thr Tyr Ser Lys Tyr Cys Glu Ala Asp Ser  
45 50 55 60  
  
gaa tgc tgt acc gaa cag tgt gta agg tct tac tgc acg ttg ttt gga 243  
Glu Cys Cys Thr Glu Gln Cys Val Arg Ser Tyr Cys Thr Leu Phe Gly  
65 70 75  
  
tgaattcgga ccacaagcca tccgatatac cccctctcct cttcagaggc ttcaaggctt 303  
ttgttatcct ttt<sup>g</sup>aagaat ct<sup>t</sup>tatcgag taaacataag tagacaagct tttttttcc 363  
tttgcaaaat gaagaatgat ggcaaaaagc cccccatttt gtcttcatca ataaagaact 423  
cgctatcaga ataaaaaa 441

<210> 21  
<211> 76  
<212> PRT  
<213> Conus textile

<400> 21  
Met Glu Lys Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Met Ser  
1 5 10 15  
Thr Gln Ala Met Phe Gln Gly Asp Gly Glu Lys Ser Arg Lys Ala Glu  
20 25 30  
Ile Asn Phe Ser Glu Thr Arg Lys Leu Ala Arg Asn Lys Gln Lys Arg  
35 40 45  
Cys Lys Thr Tyr Ser Lys Tyr Cys Glu Ala Asp Ser Glu Cys Cys Thr  
50 55 60  
Glu Gln Cys Val Arg Ser Tyr Cys Thr Leu Phe Gly  
65 70 75

<210> 22  
<211> 460  
<212> DNA  
<213> Conus textile  
  
<220>  
<221> CDS  
<222> (49) .. (273)

<400> 22  
ctgccgtcat ctcagcgcac acttggtaag aagtaaaaa ctttgcattt atg gag aaa 57  
Met Glu Lys  
1  
  
ctg aca att ctg ctt ctt gtt gct gct gtg ctg atg tcg acc cag gcc 105  
Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Met Ser Thr Gln Ala  
5 10 15  
  
cta att caa gat caa cgc caa aag gca aag atc aac ttg ttt tca aag 153  
Leu Ile Gln Asp Gln Arg Gln Lys Ala Lys Ile Asn Leu Phe Ser Lys  
20 25 30 35  
  
aga cag gca tat gct cgt gat tgg tgg gac gat ggc tgc agt gtg tgg 201  
Arg Gln Ala Tyr Ala Arg Asp Trp Trp Asp Asp Gly Cys Ser Val Trp  
40 45 50  
  
ggg cct tgt acg gtg aac gca gaa tgt tgt tct ggt gat tgt cat gaa 249  
Gly Pro Cys Thr Val Asn Ala Glu Cys Cys Ser Gly Asp Cys His Glu  
55 60 65  
  
acg tgc att ttc ggg tgg gaa gtc tgaccacaaa ccatccgaca tcggccactct 303  
Thr Cys Ile Phe Gly Trp Glu Val  
70 75  
  
cctttcaga gacttcaagg cttttgttct cttttgaaga attttacgag tgagcaaaaa 363  
ggtagactag cacgttctt tttcccttg caaatcaat gatggaggtt aaaggctccc 423  
attttgcct catcaataaa gaacttatca tcataat 460

<210> 23  
<211> 75  
<212> PRT  
<213> Conus textile  
  
<400> 23

Met Glu Lys Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Met Ser  
1 5 10 15  
Thr Gln Ala Leu Ile Gln Asp Gln Arg Gln Lys Ala Lys Ile Asn Leu  
20 25 30  
Phe Ser Lys Arg Gln Ala Tyr Ala Arg Asp Trp Trp Asp Asp Gly Cys  
35 40 45  
Ser Val Trp Gly Pro Cys Thr Val Asn Ala Glu Cys Cys Ser Gly Asp  
50 55 60  
Cys His Glu Thr Cys Ile Phe Gly Trp Glu Val  
65 70 75

<210> 24  
<211> 533  
<212> DNA  
<213> Conus textile

<220>  
<221> CDS  
<222> (110)..(337)

<400> 24  
ctctgccggt tgacacntca tctactctct cagtcctccct gacagctgcc ttcatcgac 60  
cctgcccgtca tctcagcgca gacttgataa gaagtgaaaa acctttatc atg gag aaa 118  
Met Glu Lys  
1  
ctg aca atc ctg ctt ctt gtt gct gta ctg atg tcg acc cag gcc 166  
Leu Thr Ile Leu Leu Val Ala Ala Val Leu Met Ser Thr Gln Ala  
5 10 15  
ctg gtt gaa cgt gct gga gaa aac cac tca aag gag aac atc aat ttt 214  
Leu Val Glu Arg Ala Gly Glu Asn His Ser Lys Glu Asn Ile Asn Phe  
20 25 30 35  
tta tta aaa aga aag aga gct gac agg ggg atg tgg ggc gaa tgc 262  
Leu Leu Lys Arg Lys Arg Ala Ala Asp Arg Gly Met Trp Gly Glu Cys  
40 45 50  
aaa gat ggg tta acg aca tgt ttg gcg ccc tca gag tgt tgt tct gag 310  
Lys Asp Gly Leu Thr Thr Cys Leu Ala Pro Ser Glu Cys Cys Ser Glu  
55 60 65  
gat tgt gaa ggg agc tgc acg atg tgg tgatgaattc tgaccacaag 357  
Asp Cys Glu Gly Ser Cys Thr Met Trp  
70 75  
ccatctgaca tcaccactct cctcttcaga ggctcaagg cttttgtttt cctttgaat 417  
aatctttacg agtaaacaaa taagtagact agcgcgtttt ttccctttg agaaatcaat 477  
gatggaggtta aatacgttcc tattttgtct tattcaataa agaacttatac ataata 533

<210> 25  
<211> 76  
<212> PRT  
<213> Conus textile

<400> 25

Met Glu Lys Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Met Ser  
1 5 10 15

Thr Gln Ala Leu Val Glu Arg Ala Gly Glu Asn His Ser Lys Glu Asn  
20 25 30

Ile Asn Phe Leu Leu Lys Arg Lys Arg Ala Ala Asp Arg Gly Met Trp  
35 40 45

Gly Glu Cys Lys Asp Gly Leu Thr Thr Cys Leu Ala Pro Ser Glu Cys  
50 55 60

Cys Ser Glu Asp Cys Glu Gly Ser Cys Thr Met Trp  
65 70 75

<210> 26

<211> 408

<212> DNA

<213> Conus gloriamaris

<220>

<221> CDS

<222> (2)..(211)

<400> 26

g ctg aca atc ctg ctt ctt gtt gct gct gta ctg atg tcg acc cag cag 49  
Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Met Ser Thr Gln Ala  
1 5 10 15

ctg att caa ggt ggt ggt gac aaa cgt caa aag gca aac atc aac ttt 97  
Leu Ile Gln Gly Gly Asp Lys Arg Gln Lys Ala Asn Ile Asn Phe  
20 25 30

ctt tca agg tgg gac cgt gag tgc agg gct tgg tat gcg ccg tgt agc 145  
Leu Ser Arg Trp Asp Arg Glu Cys Arg Ala Trp Tyr Ala Pro Cys Ser  
35 40 45

cct ggc gcg caa tgt tgt agt ttg ctg atg tgt tca aaa gcg acc agc 193  
Pro Gly Ala Gln Cys Cys Ser Leu Leu Met Cys Ser Lys Ala Thr Ser  
50 55 60

cgc tgc ata ttg gcg tta tgaactctga ccacaaggcca tccgacatca 241  
Arg Cys Ile Leu Ala Leu  
65 70

ccactctcct cttcagagggc ttcaaggctt ttgttttc ttttgaagaa tctttacgag 301

tgaacaaata agtagaataag cacgttttc ccccttgca aaatcaataa tggaggttaa 361

aaaaaaaaactt ctgtcttctt caataaaagaa gttatcataa taaaaaaaa 408

<210> 27

<211> 70

<212> PRT

<213> Conus gloriamaris

<400> 27

Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Met Ser Thr Gln Ala  
1 5 10 15

Leu Ile Gln Gly Gly Asp Lys Arg Gln Lys Ala Asn Ile Asn Phe

20

25

30

Leu Ser Arg Trp Asp Arg Glu Cys Arg Ala Trp Tyr Ala Pro Cys Ser  
35 40 45

Pro Gly Ala Gln Cys Cys Ser Leu Leu Met Cys Ser Lys Ala Thr Ser  
50 55 60

Arg Cys Ile Leu Ala Leu  
65 70

<210> 28

<211> 278

<212> DNA

<213> Conus marmoreus

<220>

<221> CDS

<222> (4)..(222)

<400> 28

atc atg cag aaa ctg ata atc ctg ctt ctt gtt gct gct gtg ctg ctg  
Met Gln Lys Leu Ile Ile Leu Leu Leu Val Ala Ala Val Leu Leu  
1 5 10 15

48

tcg acc cag gcc cta aat caa gaa aaa cgc cca aag gag atg atc aat  
Ser Thr Gln Ala Leu Asn Gln Glu Lys Arg Pro Lys Glu Met Ile Asn  
20 25 30

96

ttt tta tca aaa gga aag aca aat gct gag agg cgg aac ggc caa tgc  
Phe Leu Ser Lys Gly Lys Thr Asn Ala Glu Arg Arg Asn Gly Gln Cys  
35 40 45

144

gag gat gtt tgg atg cct tgt aca tcg aac tgg gaa tgc tgt tct ttg  
Glu Asp Val Trp Met Pro Cys Thr Ser Asn Trp Glu Cys Cys Ser Leu  
50 55 60

192

gat tgt gaa atg tac tgc aca cag ata gga tgaactctga ccacaaggcca  
Asp Cys Glu Met Tyr Cys Thr Gln Ile Gly  
65 70

242

tccgacatca ccactctcct cttcagagtc ttcaag 278

<210> 29

<211> 73

<212> PRT

<213> Conus marmoreus

<400> 29

Met Gln Lys Leu Ile Ile Leu Leu Leu Val Ala Ala Val Leu Leu Ser  
1 5 10 15

Thr Gln Ala Leu Asn Gln Glu Lys Arg Pro Lys Glu Met Ile Asn Phe  
20 25 30

Leu Ser Lys Gly Lys Thr Asn Ala Glu Arg Arg Asn Gly Gln Cys Glu  
35 40 45

Asp Val Trp Met Pro Cys Thr Ser Asn Trp Glu Cys Cys Ser Leu Asp  
50 55 60

Cys Glu Met Tyr Cys Thr Gln Ile Gly

65

70

<210> 30  
<211> 287  
<212> DNA  
<213> Conus marmoreus

<220>  
<221> CDS  
<222> (4) .. (231)

<400> 30

atc atg gag aaa ctg aca atc ctg ctt gtt gct gct gta ctg ata 48  
Met Glu Lys Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Ile  
1 5 10 15

ccg acc cag gcc ctt ttt caa ggt gat gac gga aaa tcc cag aag gcg 96  
Pro Thr Gln Ala Leu Phe Gln Gly Asp Asp Gly Lys Ser Gln Lys Ala  
20 25 30

gag atc aag tct ttt gaa aca aga aag tta gcg aga aac aag cag gta 144  
Glu Ile Lys Ser Phe Glu Thr Arg Lys Leu Ala Arg Asn Lys Gln Val  
35 40 45

cgc tgc ggt ggt tgg tca acg tat tgt gaa gtt gac gag gaa tgc tgt 192  
Arg Cys Gly Trp Ser Thr Tyr Cys Glu Val Asp Glu Glu Cys Cys  
50 55 60

tcg gaa tca tgt gta agg tct tac tgc acg ctg ttt gga tgaactcgga 241  
Ser Glu Ser Cys Val Arg Ser Tyr Cys Thr Leu Phe Gly  
65 70 75

ccacaaggcca tccgatataca ccactctcct gttcagagtc ttcaag 287

<210> 31  
<211> 76  
<212> PRT  
<213> Conus marmoreus

<400> 31  
Met Glu Lys Leu Thr Ile Leu Leu Val Ala Ala Val Leu Ile Pro  
1 5 10 15

Thr Gln Ala Leu Phe Gln Gly Asp Asp Gly Lys Ser Gln Lys Ala Glu  
20 25 30

Ile Lys Ser Phe Glu Thr Arg Lys Leu Ala Arg Asn Lys Gln Val Arg  
35 40 45

Cys Gly Gly Trp Ser Thr Tyr Cys Glu Val Asp Glu Glu Cys Cys Ser  
50 55 60

Glu Ser Cys Val Arg Ser Tyr Cys Thr Leu Phe Gly  
65 70 75

<210> 32  
<211> 278  
<212> DNA  
<213> Conus marmoreus

<220>

<221> CDS

<222> (4)..(213)

<400> 32

atc atg cag aaa ctg ata att ctg ctt ctt gtt gct gct gtg ctg atg	48
Met Gln Lys Leu Ile Ile Leu Leu Leu Val Ala Ala Val Leu Met	
1 5 10 15	

acg acc cag gcc cta tat caa gaa aaa cgc cga aag gag atg atc aat	96
Thr Thr Gln Ala Leu Tyr Gln Glu Lys Arg Arg Lys Glu Met Ile Asn	
20 25 30	

ttt tta tca aaa gga aag ata aat gct gag agg cgg aac ggc gga tgc	144
Phe Leu Ser Lys Gly Lys Ile Asn Ala Glu Arg Arg Asn Gly Gly Cys	
35 40 45	

aaa gct act tgg atg tct tgt tca tcg ggc tgg gaa tgc tgt tct atg	192
Lys Ala Thr Trp Met Ser Cys Ser Ser Gly Trp Glu Cys Cys Ser Met	
50 55 60	

agt tgt gac atg tac tgc gga tagataggat gaactctgac cacaagccat	243
Ser Cys Asp Met Tyr Cys Gly	
65 70	

ccgacatcac cactctcctc ttcagagtct tcaag 278

<210> 33

<211> 70

<212> PRT

<213> Conus marmoreus

<400> 33

Met Gln Lys Leu Ile Ile Leu Leu Leu Val Ala Ala Val Leu Met Thr	
1 5 10 15	

Thr Gln Ala Leu Tyr Gln Glu Lys Arg Arg Lys Glu Met Ile Asn Phe	
20 25 30	

Leu Ser Lys Gly Lys Ile Asn Ala Glu Arg Arg Asn Gly Gly Cys Lys	
35 40 45	

Ala Thr Trp Met Ser Cys Ser Ser Gly Trp Glu Cys Cys Ser Met Ser	
50 55 60	

Cys Asp Met Tyr Cys Gly

<210> 34

<211> 528

<212> DNA

<213> Conus textile

<220>

<221> CDS

<222> (98)..(316)

<400> 34

gcacgtcatc ttctctctca gtctgcctga cagctgcctt cagtcacacc tgccgtcatc 60

tcagcgtaga cttggtaaga agtgaaaaac atttatac atg cag aaa ctg ata atc	115
Met Gln Lys Leu Ile Ile	
1 5	

ctg ctt ctt gtt gct gct gtg	ctg atg tcg acc cag gcc	gtg ctt caa	163
Leu Leu Leu Val Ala Ala Val	Leu Met Ser Thr Gln Ala	Val Leu Gln	
10	15	20	
gaa aaa cgc cca aag gag aag	atc aag ctt tta tca aag	aga aag aca	211
Glu Lys Arg Pro Lys Glu Lys	Ile Lys Leu Leu Ser	Lys Arg Lys Thr	
25	30	35	
gat gct gag aag cag cag aag	cgc ctt tgc ccg gat tac	acg gag cct	259
Asp Ala Glu Lys Gln Gln	Lys Arg Leu Cys Pro Asp	Tyr Thr Glu Pro	
40	45	50	
tgt tca cat gcc cat gaa tgc	tgt tca tgg aat tgc aat	tat aat ggg cac	307
Cys Ser His Ala His Glu Cys	Cys Ser Trp Asn Cys	Tyr Asn Gly His	
55	60	65	70
tgt acg gga tgaactcgga ccacaagcca	tccgacatca ccactctcct		356
Cys Thr Gly			
cttcagaggc ttcaagactt ttgttctgat	tttggacaat cttagcagt	aaacaaataa	416
ttagactagc acttttttc cccttgcaa aatcaatgat	ggaggtaaaa agcctcccat		476
tttgtcttca tcaataaaaga acttatcatc	aaaaaaaaaa aaaaaaaaaa	aa	528

<210> 35  
<211> 73  
<212> PRT  
<213> Conus textile

<400> 35  
Met Gln Lys Leu Ile Ile Leu Leu Leu Val Ala Ala Val Leu Met Ser  
1 5 10 15  
Thr Gln Ala Val Leu Gln Glu Lys Arg Pro Lys Glu Lys Ile Lys Leu  
20 25 30  
Leu Ser Lys Arg Lys Thr Asp Ala Glu Lys Gln Gln Lys Arg Leu Cys  
35 40 45  
Pro Asp Tyr Thr Glu Pro Cys Ser His Ala His Glu Cys Cys Ser Trp  
50 55 60  
Asn Cys Tyr Asn Gly His Cys Thr Gly  
65 70

<210> 36  
<211> 26  
<212> PRT  
<213> Conus textile

<220>  
<221> PEPTIDE  
<222> (1)..(26)  
<223> Xaa at residue 18 is Trp or 6-bromo-Trp; Xaa at  
residues 7 and 14 are Glu or  
gamma-carboxyglutamate; Xaa at residues 3 and 8  
are Pro or hydroxy-Pro.

<400> 36  
Leu Cys Xaa Asp Tyr Thr Xaa Xaa Cys Ser His Ala His Xaa Cys Cys  
1 5 10 15

Ser Xaa Asn Cys Tyr Asn Gly His Cys Thr  
20 25

<210> 37  
<211> 4  
<212> PRT  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence:consensus  
gamma-conopeptide sequence for probe  
  
<220>  
<221> PEPTIDE  
<222> (1)  
<223> Xaa is Glu or Gln.

<400> 37  
Xaa Cys Cys Ser  
1

<210> 38  
<211> 12  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence:degenerate  
probe for consensus gamma-conopeptide sequence.

<400> 38  
sartgytgya gy

12

<210> 39  
<211> 12  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence:degenerate  
probe for consensus gamma-conopeptide sequence.

<400> 39  
sartgytgyt cn

12

<210> 40  
<211> 8  
<212> PRT  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence:consensus  
pro-gamma-conopeptide sequence for probe.

<400> 40  
Ile Leu Leu Val Ala Ala Val Leu  
1 5

<210> 41

<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:degenerate  
probe for consensus pro-gamma-conopeptide  
sequence.

<400> 41  
athytnytnng tngcngcngt nytn

24

<210> 42  
<211> 32  
<212> PRT  
<213> Conus pennaceus

<220>  
<221> PEPTIDE  
<222> (1)..(31)  
<223> Xaa at residues 14 and 26 are  
gamma-carboxyglutamate; Xaa at residue 31 is  
hydroxy-Pro.

<400> 42  
Asp Cys Thr Ser Trp Phe Gly Arg Cys Thr Val Asn Ser Xaa Cys Cys  
1 5 10 15  
Ser Asn Ser Cys Asp Gln Thr Tyr Cys Xaa Leu Tyr Ala Phe Xaa Ser  
20 25 30

<210> 43  
<211> 27  
<212> PRT  
<213> Conus textile

<220>  
<221> PEPTIDE  
<222> (1)..(27)  
<223> Xaa at residues 9 and 13 are  
gamma-carboxyglutamate.

<400> 43  
Cys Gly Gly Tyr Ser Thr Tyr Cys Xaa Val Asp Ser Xaa Cys Cys Ser  
1 5 10 15  
Asp Asn Cys Val Arg Ser Tyr Cys Thr Leu Phe  
20 25

<210> 44  
<211> 8  
<212> PRT  
<213> Conus pennaceus

<220>  
<221> MOD\_RES  
<222> (2)  
<223> Xaa at residue 2 is carboxymethylCys

<400> 44  
Asp Xaa Thr Ser Trp Phe Gly Arg  
1 5

<210> 45  
<211> 24  
<212> PRT  
<213> Conus pennaceus

<220>  
<221> PEPTIDE  
<222> (1)..(24)  
<223> Xaa at residues 6 and 18 are  
gamma-carboxyglutamate; Xaa at residue 23 is  
hydroxy-Pro.

<400> 45  
Xaa Thr Val Asn Ser Xaa Xaa Xaa Ser Asn Ser Xaa Asp Gln Thr Tyr  
1 5 10 15  
Xaa Xaa Leu Tyr Ala Phe Xaa Ser  
20

<210> 46  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer for M13  
universal priming site.

<400> 46  
tttcccagtc acgacgtt 18

<210> 47  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer for M13  
reverse priming site.

<400> 47  
cacacaggaa acagctatg 19